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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/970,969

DATE: 10/19/2001

TIME: 10:33:27

Input Set : A:\PTO_VSK.txt

Output Set: N:\CRF3\10192001\I970969.raw

3 <110> APPLICANT: Tait, Jonathan F.
5 Brown, David S.
9 <120> TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites
13 <130> FILE REFERENCE: uofw-1-13841
C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/970,969
C--> 19 <141> CURRENT FILING DATE: 2001-10-03
23 <160> NUMBER OF SEQ ID NOS: 6
27 <170> SOFTWARE: PatentIn Ver. 2.0
31 <210> SEQ ID NO: 1
33 <211> LENGTH: 981
35 <212> TYPE: DNA
37 <213> ORGANISM: Homo sapiens
41 <220> FEATURE:
43 <221> NAME/KEY: CDS
45 <222> LOCATION: (1)..(981)
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61 Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg
63 20 25 30
67 aag gct atg aaa ggc ttg ggc aca gat gag gag agc atc ctg act ctg 144
69 Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu
71 35 40 45
75 ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt 192
77 Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe
79 50 55 60
83 aag act ctg ttt ggc agg gat ctt ctg gat gac ctg aaa tca gaa cta 240
85 Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu
87 65 70 75 80
91 act gga aaa ttt gaa aaa tta att gtg gct ctg atg aaa ccc tct cgg 288
93 Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
95 85 90 95
99 ctt tat gat gct tat gaa ctg aaa cat gcc ttg aag gga gct gga aca 336
101 Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr
103 100 105 110
107 aat gaa aaa gta ctg aca gaa att att gct tca agg aca cct gaa gaa 384
109 Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
111 115 120 125
115 ctg aga gcc atc aaa caa gtt tat gaa gaa gaa tat ggc tca agc ctg 432
117 Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu
119 130 135 140
123 gaa gat gac gtg gtg ggg gac act tca ggg tac tac cag cgg atg ttg 480
125 Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu
127 145 150 155 160
131 gtg gtt ctc ctt cag gct aac aga gac cct gat gct gga att gat gaa 528

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147 aaa tgg ggg aca gat gaa gaa aag ttt atc acc atc ttt gga aca cga 624
149 Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg
151                               195                               200                               205
155 agt gtg tct cat ttg aga aag gtg ttt gac aag tac atg act ata tca 672
157 Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser
159                               210                               215                               220
163 gga ttt caa att gag gaa acc att gac cgc gag act tct ggc aat tta 720
165 Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu
167 225                               230                               235                               240
171 gag caa cta ctc ctt gct gtt gtg aaa tct att cga agt ata cct gcc 768
173 Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala
175                               245                               250                               255
179 tac ctt gca gag acc ctc tat tat gct atg aag gga gct ggg aca gat 816
181 Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp
183                               260                               265                               270
187 gat cat acc ctc atc aga gtc atg gtt tcc agg agt gag att gat ctg 864
189 Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
191                               275                               280                               285
195 ttt aac atc agg aag gag ttt agg aag aat ttt gcc acc tct ctt tat 912
197 Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr
199                               290                               295                               300
203 tcc atg att aag gga gat aca tct ggg gac tat aag aaa gct ctt ctg 960
205 Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu
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245 Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu
247 35 40 45
251 Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe
253 50 55 60
257 Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu
259 65 70 75 80
263 Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
265 85 90 95

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275 Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
277      115      120      125
281 Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu
283      130      135      140
287 Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu
289 145      150      155      160
293 Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu
295      165      170      175
299 Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu
301      180      185      190
305 Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg
307      195      200      205
311 Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser
313      210      215      220
317 Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu
319 225      230      235      240
323 Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala
325      245      250      255
329 Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp
331      260      265      270
335 Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
337      275      280      285
341 Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr
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347 Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu
349 305      310      315      320
353 Leu Leu Ser Gly Glu Asp Asp
355      325
361 <210> SEQ ID NO: 3
363 <211> LENGTH: 981
365 <212> TYPE: DNA
367 <213> ORGANISM: Homo sapiens
371 <220> FEATURE:
373 <221> NAME/KEY: CDS
375 <222> LOCATION: (1)..(981)
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385 1 5 10 15
389 act gac ttc cct gga ttt gat gag cgg gct gat gca gaa act ctt cgg 96
391 Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg
393 20 25 30
397 aag gct atg aaa ggc ttg ggc aca gat gag gag agc atc ctg act ctg 144
399 Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu
401 35 40 45
405 ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt 192
407 Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe

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413	aag act ctg ttt ggc agg gat ctt ctg gat gac ctg aaa tca gaa cta	240		
415	Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu			
417	65	70	75	80
421	act gga aaa ttt gaa aaa tta att gtg gct ctg atg aaa ccc tct cgg	288		
423	Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg			
425		85	90	95
429	ctt tat gat gct tat gaa ctg aaa cat gcc ttg aag gga gct gga aca	336		
431	Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr			
433		100	105	110
437	aat gaa aaa gta ctg aca gaa att att gct tca agg aca cct gaa gaa	384		
439	Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu			
441		115	120	125
445	ctg aga gcc atc aaa caa gtt tat gaa gaa gaa tat gcc tca agc ctg	432		
447	Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu			
449		130	135	140
453	gaa gat gac gtg gtg ggg gac act tca ggg tac tac cag cgg atg ttg	480		
455	Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu			
457	145	150	155	160
461	gtg gtt ctc ctt cag gct aac aga gac cct gat gct gga att gat gaa	528		
463	Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu			
465		165	170	175
469	gct caa gtt gaa caa gat gct cag gct tta ttt cag gct gga gaa ctt	576		
471	Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu			
473		180	185	190
477	aaa tgg ggg aca gat gaa gaa aag ttt atc acc atc ttt gga aca cga	624		
479	Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg			
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485	agt gtg tct cat ttg aga aag gtg ttt gac aag tac atg act ata tca	672		
487	Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser			
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493	gga ttt caa att gag gaa acc att gac cgc gag act tct ggc aat tta	720		
495	Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu			
497	225	230	235	240
501	gag caa cta ctc ctt gct gtt gtg aaa tct att cga agt ata cct gcc	768		
503	Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala			
505		245	250	255
509	tac ctt gca gag acc ctc tat tat gct atg aag gga gct ggg aca gat	816		
511	Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp			
513		260	265	270
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521		275	280	285
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535	Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu			
537	305	310	315	320

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541 ctg ctc tcc gga gaa gat gac          981
543 Leu Leu Ser Gly Glu Asp Asp
545                               325
551 <210> SEQ ID NO: 4
553 <211> LENGTH: 327
555 <212> TYPE: PRT
557 <213> ORGANISM: Homo sapiens
561 <400> SEQUENCE: 4
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565   1           5           10           15
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571           20           25           30
575 Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu
577           35           40           45
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593 Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg
595           85           90           95
599 Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr
601           100          105          110
605 Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu
607           115          120          125
611 Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu
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623 Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu
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629 Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu
631           180          185          190
635 Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg
637           195          200          205
641 Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser
643           210          215          220
647 Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu
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661           260          265          270
665 Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu
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673           290          295          300
677 Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu
679 305          310          315          320
683 Leu Leu Ser Gly Glu Asp Asp

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VERIFICATION SUMMARY

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L:17 M:270 C: Current Application Number differs, Replaced Application Number

L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date